Abstract: *Xylella fastidiosa* is a gram-negative pathogen that causes disease in a wide variety of agriculturally significant plants, such as olive, almond and cherry trees, to name a few. The pathogen poses a great threat to the UK as many of its host plants are found here. The present study attempts to understand the genetics behind the different subspecies of *X. fastidiosa* by means of population genomics. There are currently 46 publicly available genomes. A pipeline is being developed to identify factors that aid in the virulence of the bacterium, which will then be implemented for a larger population.

This research may gain more insight into the complex host range of the bacterium, its yet unknown mode of action within the plant, and determine why the pathogen causes disease in some hosts but remains asymptomatic in others. Ultimately, the outcome of the study could pave the way to implementing further control measures and creating diagnostic tools for the prevention of an outbreak.

Screening olive germplasm for resistance to olive quick decline syndrome caused by *Xylella fastidiosa* under field and controlled conditions

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Abstract: Searching for resistance is regarded as one of the most promising long-term control strategies against the olive quick decline syndrome (OQDS) caused by *Xylella fastidiosa* (Xf). A set of 60 olive genotypes are now being screened for resistance to OQDS under field and controlled conditions. Plants consisted of self-rooted plants, produced at IFAPA in Córdoba (Spain) and then transferred to the CNR-IPSP-Bari (Italy). A first batch of 10 genotypes from different *Olea europaea* subspecies and 10 breeding selections from the IFAPA breeding programme was planted in open field under high disease pressure in November 2016 and inoculated under controlled greenhouse conditions in March 2017. A second batch of 40 cultivars selected from the World Olive Germplasm Collection, representative of the genetic and geographical variability of the collection, was inoculated under controlled greenhouse conditions and exposed to natural infections in summer 2017. Preliminary results indicate differences in the incidences of the infections and, among those that support systemic infections, differences were recorded for the presence and severity of shoot dieback and desiccation phenomena. Results gathered under controlled conditions allowed to identify some genotypes in which poor systemic infections (only few replicates were colonised) were detected even upon two rounds of inoculations. Conversely, symptoms of shoot dieback were recorded on some accessions, most probably indicating they are particularly sensitive to the infections. Interestingly, the selection of Leccino confirmed previous evidence, with inoculated plants harbouring low bacterial population size and not showing severe shoot dieback. However, especially for the field experiments affected by the weather and climatic conditions, observations and quantitative assays need to be prolonged in order to acquire conclusive data from multi-year surveys. On the basis of these preliminary results, a first set of progenies from tentative resistant genitors are being currently developed for future studies.

Genomic insights into the diversity of European *Xylella fastidiosa* isolates

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Abstract: A growing number of recent and current studies on *Xylella fastidiosa* outbreaks in Europe emphasise genomic sequencing of bacterial isolates as a mean to infer their

potential origin, biology, recombination events and possible determinants of host specificity.

In the present work we have undertaken a re-assessment of publicly available *X. fastidiosa* genomic sequences from a comparative standpoint. With limitations due to the fact that most of the available sequences were left at the draft stage, and that only a few are complete, we undertook to compare: i) genomic organisation (synteny); ii) number, origin and genomic position of insertion elements (IS, islands, phage-related elements, plasmids); iii) individual gene complements within the species and subspecies pan-genomes; and iv) exclusive or enriched genes associated with subspecies or host of isolation. Our preliminary results suggest that *X. fastidiosa* genomes show a great plasticity in their organisation, possibly aided by the widespread presence of insertion elements, and that the traditional subspecies classification, although useful from an operational standpoint, is probably insufficient to explain the observed genomic variability.

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A global map of *Xylella* plasmidome reveals broad host and geographical distribution

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Abstract: Despite the knowledge generated on *Xylella fastidiosa* (Xf), the contribution of mobile genetic elements to its biology remains unveiled. Conjugative elements, in addition to its role in genetic transfer, are involved in bacterial adhesion and biofilm formation. One of the main difficulties to treat Xf is linked to its ability to form biofilms, both in the plant xylem and in the insect vectors. Previous studies reported the existence of different plasmids in Xf; however, their functions, distribution and host range have not been globally characterised. Here, by analysing plasmid genomic composition and sequence homology, we infer a global map of the *Xylella* plasmidome.

Our genomic analysis found that almost all Xf sequenced strains carry at least a potentially conjugative plasmid encoding a relaxase (belonging to the MOBP family), a coupling protein and a complete T4SS (generally belonging to the MPFT type). Furthermore, half of these plasmids harbour at least a virulence-coding gene, most of them putatively involved in cell adhesion. Analysis of Xf plasmids by average nucleotide identity levels unveiled that they organised into a few discrete coherent genomic clusters, that we called plasmid taxonomic units (pTUs). Interestingly, some clusters were restricted to a single Xf host, while other pTUs have colonised all subspecies, indicating that they can be directly exchanged and spread among them. The homologous protein network analysis showed the proteome specificities and commonalities of Xf pTUs. Considering that conjugation involves co-occurrence of donor and receptor cells in the same ecological niche, our analysis sheds light on *Xylella* evolutionary history and geographic distribution.

Phylogenomic analysis of the species *Xylella fastidiosa*

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Abstract: *Xylella fastidiosa* is a phytopathogenic bacterium considered as a quarantine pathogen for the EU that affects a broad spectrum of hosts. It has stood out in recent years due to its detection in the EU, especially in Italy, the Balearic Islands, Alicante and Corsica. It has important environmental implications and is the cause of millionaire agricultural losses.